

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg	403
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr	
90	95
	100
cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct	451
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala	
105	110
	115
tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct	499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala	
120	125
	130
ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct	547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala	
135	140
	145
act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc	595
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala	
150	155
	160
	165
gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct	643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala	
170	175
	180
tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc	691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe	
185	190
	195
gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa	739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys	
200	205
	210
gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg	787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly	
215	220
	225
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca	835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr	
230	235
	240
	245
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt	883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe	
250	255
	260
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac	931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn	
265	270
	275
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag	979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys	
280	285
	290
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt	1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu	
295	300
	305

caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn 310 315 320 325	1075
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val 330 335 340	1123
gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser 345 350 355	1171
atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser 360 365 370	1219
ggg ttt cgt cag att cac atg ttc aat acg gaa aat cct gat tct Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser 375 380 385	1267
caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala 390 395 400 405	1315
gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct Ala Gly Asp Asp Ser Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala 410 415 420	1363
tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat Leu Glu Ala Ala Leu Gly Ala Gly Gln Gln Gln Gly Ile Leu Asn 425 430 435	1411
gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt cct Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro 440 445 450	1459
ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Val Lys Gln Leu Tyr Lys 455 460 465	1507
acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly 470 475 480 485	1555
tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga aat Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn 490 495 500	1603
gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc aca Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr 505 510 515	1651
cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr 520 525 530	1699

gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt gga Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly 535 540 545	1747
gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile 550 555 560 565	1795
cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr 570 575 580	1843
tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu 585 590 595	1891
tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe 600 605 610	1939
gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu 615 620 625	1987
acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu 630 635 640 645	2035
tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga Tyr Ser Gly Tyr Leu Gln 650	2083
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aataaaataaa aga	2156

<210> 2
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<212> PRT
<213> Chlamydia pneumoniae

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Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn 20 25 30
Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys 35 40 45
Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala 50 55 60

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Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
65 70 75 80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr
85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr
100 105 110

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala
115 120 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile
130 135 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp
145 150 155 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu
165 170 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly
180 185 190

Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val
195 200 205

Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn
210 215 220

Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp
225 230 235 240

Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile
245 250 255

Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn
260 265 270

Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala
275 280 285

Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro
290 295 300

Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu
305 310 315 320

Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn
325 330 335

Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly
340 345 350

TOPIC: OMEGAGENOTEST

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Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala
355 360 365

Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr
370 375 380

Glu Asn Pro Asp Ser Gln Ala Ala Gln Glu Leu Ala Ala Gln Ala
385 390 395 400

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
405 410 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
420 425 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val
435 440 445

Ser Ala Gly Val Pro Pro Ala Ala Ser Ser Ile Gly Ser Ser Val
450 455 460

Lys Gln Leu Tyr Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr
465 470 475 480

Gln Ile Ser Ala Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr
485 490 495

Gly Arg Ala Arg Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser
500 505 510

Thr Pro Ala Leu Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg
515 520 525

Gly Pro Glu Lys Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn
530 535 540

Ser Arg Thr Leu Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser
545 550 555 560

Val Met Gln Ile Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile
565 570 575

Arg Gln Lys Leu Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr
580 585 590

Pro Tyr Val Gln Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys
595 600 605

Leu Glu Ser Leu Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys
610 615 620

Ala Leu Ser Phe Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val
625 630 635 640

Asn Ile Gly Ser Leu Tyr Ser Gly Tyr Leu Gln
645 650

<210> 3

<211>

<212> DNA

<213> Chlamydia pneumoniae

<220> 1842

<221> CDS

<222> (101..(2053)

<400> 3

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Met	Ser	Leu	Ala	Asp	Lys	Leu	Gly	Ile	Ala	Ser	Ser	Asn	Ser	Ser	Ser		
1	5								10						15		

tct	act	agc	aga	tct	gca	gac	gtg	gac	tca	acg	aca	gcg	acc	gca	cct		96
Ser	Thr	Ser	Arg	Ser	Ala	Asp	Val	Asp	Ser	Thr	Thr	Ala	Thr	Ala	Pro		
20		25								30							

acg	cct	cca	ccc	acg	ttt	gat	gat	tat	aag	act	caa	gcg	caa	aca		144
Thr	Pro	Pro	Pro	Pro	Phe	Asp	Asp	Tyr	Lys	Thr	Gln	Ala	Gln	Thr		
35		40							45							

gct	tac	gat	act	atc	ttt	acc	tca	aca	tca	cta	gct	gac	ata	cag	gct		192
Ala	Tyr	Asp	Thr	Ile	Phe	Thr	Ser	Thr	Ser	Leu	Ala	Asp	Ile	Gln	Ala		
50			55						60								

gct	ttg	gtg	agc	ctc	cag	gat	gct	gtc	act	aat	ata	aag	gat	aca	gcg		240
Ala	Leu	Val	Ser	Leu	Gln	Asp	Ala	Val	Thr	Asn	Ile	Lys	Asp	Thr	Ala		
65			70						75			80					

gct	act	gat	gag	gaa	acc	gca	atc	gct	gcg	gag	tgg	gaa	act	aag	aat		288
Ala	Thr	Asp	Glu	Glu	Thr	Ala	Ile	Ala	Ala	Glu	Trp	Glu	Thr	Lys	Asn		
85			90							95							

gcc	gat	gca	gtt	aaa	gtt	ggc	gcf	caa	att	aca	gaa	tta	gcf	aaa	tat		336
Ala	Asp	Ala	Val	Lys	Val	Gly	Ala	Gln	Ile	Thr	Glu	Leu	Ala	Lys	Tyr		
100				105						110							

gct	tcg	gat	aac	caa	gcf	att	ctt	gac	tct	tta	ggt	aaa	ctg	act	tcc		384
Ala	Ser	Asp	Asn	Gln	Ala	Ile	Leu	Asp	Ser	Leu	Gly	Lys	Leu	Thr	Ser		
115			120							125							

ttc	gac	ctc	tta	cag	gct	ctt	ctc	caa	tct	gta	gca	aac	aat	aac		432
Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	Ala	Asn	Asn	Asn	
130			135							140						

aaa	gca	gct	gag	ctt	aaa	gag	atg	caa	gat	aac	cca	gta	gtc	cca		480
Lys	Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	Pro	Val	Val	Pro	
145			150						155			160				

ggg	aaa	acg	cct	gca	att	gct	caa	tct	tta	gtt	gat	cag	aca	gat	gct		528
Gly	Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	Gln	Thr	Asp	Ala		
165			170							175							

4000146200 - 12 - 100

aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat 576
 Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr
 180 190 195

 ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat 624
 Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn
 200 205 210

 aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct 672
 Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala
 215 220 225

 aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att 720
 Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile
 230 235 240 245

 ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa 768
 Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys
 250 255 260

 aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca 816
 Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr
 265 270 275

 gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt 864
 Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val
 280 285 290

 tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg 912
 Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met
 295 300 305

 tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat 960
 Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp
 310 315 320 325

 tct caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa 1008
 Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys
 330 335 340

 gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa 1056
 Ala Ala Gly Asp Asp Ser Ala Ala Ala Leu Ala Asp Ala Gln Lys
 345 350 355

 gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc 1104
 Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gly Ile Leu
 360 365 370

 aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt 1152
 Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val
 375 380 385

 CCt ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac 1200
 Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Val Lys Gln Leu Tyr
 390 395 400 405

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aag acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca 1248
Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala
410 415 420

ggt tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga 1296
Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg
425 430 435

aat gat gcg act cgt gat gtg at aac aat gta agt acc ccc gct ctc 1344
Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu
440 445 450

aca cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa 1392
Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys
455 460 465

aca gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt 1440
Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu
470 475 480 485

gga gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc 1488
Gly Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile
490 495 500

act cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt 1536
Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu
505 510 515

aca tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa 1584
Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln
520 525 530

ctt tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg 1632
Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu
535 540 545

ttt gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt 1670
Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe
550 555 560 565

gaa acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct 1718
Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser
570 575 580

cta tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 1769
Leu Tyr Ser Gly Tyr Leu Gln
585

ttattatgtg ctttgtaag gccttttgttggaggccttacc aacacacttag aacgatcttc 1829

aataaaataaa aga 1842

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<210> 4

<211> 583

<212> PRT

<213> Chlamydia pneumoniae

<400> 4

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20 25 30

Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr
35 40 45

Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala
50 55 60

Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala
65 70 75 80

Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn
85 90 95

Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr
100 105 110

Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser
115 120 125

Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn
130 135 140

Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro
145 150 155 160

Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala
165 170 175

Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr
180 185 190

Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn
195 200 205

Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala
210 215 220

Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile
225 230 235 240

Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys
245 250 255

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Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr
260 265 270

Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val
275 280 285

Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met
290 295 300

Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp
305 310 315 320

Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys
325 330 335

Ala Ala Gly Asp Asp Ser Ala Ala Ala Leu Ala Asp Ala Gln Lys
340 345 350

Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gly Ile Leu
355 360 365

Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val
370 375 380

Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr
385 390 395 400

Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala
405 410 415

Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg
420 425 430

Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu
435 440 445

Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys
450 455 460

Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu
465 470 475 480

Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile
485 490 495

Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu
500 505 510

Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln
515 520 525

Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu
530 535 540

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Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe
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Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser
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Leu Tyr Ser Gly Tyr Leu Gln
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<210> 5

<211> 1456

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (101)..(1456)

<400> 5

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Met Val Asn Pro Ile
1 5

ggc cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt 163
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu
10 15 20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct 211
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala
25 30 35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat 259
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp
40 45 50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg 307
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met
55 60 65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct 355
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser
70 75 80 85

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg 403
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr
90 95 100

cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct 451
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala
105 110 115

4041463701

tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct		499	
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala			
120	125	130	
ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct		547	
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala			
135	140	145	
act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc		595	
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala			
150	155	160	165
gat gca gtt aaa gtt gg ^c gcg caa att aca gaa tta gcg aaa tat gct		643	
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala			
170	175	180	
tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc		691	
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe			
185	190	195	
gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa		739	
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys			
200	205	210	
gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg		787	
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly			
215	220	225	
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca		835	
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr			
230	235	240	245
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt		883	
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe			
250	255	260	
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac		931	
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn			
265	270	275	
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag		979	
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys			
280	285	290	
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt		1027	
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu			
295	300	305	
caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat		1075	
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn			
310	315	320	325
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt		1123	
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val			
330	335	340	

gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc	1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser	
345	350
355	
atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct	1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser	
360	365
370	
ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct	1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser	
375	380
385	
caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc	1315
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala	
390	395
400	405
gct gga gat gac agt gct gca gcg ctg gca gat gct cag aaa gct	1363
Ala Gly Asp Asp Ser Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala	
410	415
420	
tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat	1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn	
425	430
435	
gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta	1456
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val	
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<212> PRT

<213> Chlamydia pneumoniae

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Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys	
35	40
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Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala	
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60	

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser	
65	70
75	80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr	
85	90
95	

Ala Thr Ala Pro Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr	
100	105
110	

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala
 115 120 125
 Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile
 130 135 140
 Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp
 145 150 155 160
 Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu
 165 170 175
 Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly
 180 185 190
 Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val
 195 200 205
 Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn
 210 215 220
 Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp
 225 230 235 240
 Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile
 245 250 255
 Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn
 260 265 270
 Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala
 275 280 285
 Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro
 290 295 300
 Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu
 305 310 315 320
 Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn
 325 330 335
 Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly
 340 345 350
 Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala
 355 360 365
 Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr
 370 375 380
 Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala
 385 390 395 400

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala
 405 410 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
 420 425 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val
 435 440 445

Ser Ala Gly Val
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<210> 7

<211> 2238

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (766)..(2235)

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acagaaaaaaag ctgctacaaa cgctatgaaa tacaaatact gtgtttggca gtggctcgtc 180

ggaaagcata gtcaggttcc ttggatcaat ggacagaaaaa agcctctata tctttatgga 240

gctttcttaa tgaacccttt agcaaaggct acgaagacta cgttaaatgg aaaagaaaaac 300

ctagcttggt ttattggagg aacttttaggg ggactcagaa aagctggaga ctggctcgcc 360

acagtacgtt atgagtagtgt cgaagccttg tcggttccag aaatagatgt ttcagggatt 420

ggccgtggta atttattaaa gttttggttc gcccaagcaa ttgctgctaa ctatgatcct 480

aaagaggcta atggttttac aaattataaa ggattttcccg ctcttatatat gtatggcatc 540

acagattctc tatcatttcag agctttaggg gcttactcca aaccagcaaa cgataaaactc 600

ggcagtgatt ttactttccg aaagtttgat ctaggtataaa tttcagcggt ttaagtcaaa 660

ttttataataa atctttaaaaa acaggctcgc attaattatt agtgagagct ttttttttat 720

ttttataata aaaaactaaaaa gatttttatt attttttgag ttttt atg gtt aat cct 777

Met Val Asn Pro

1

att ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat 825
 Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp

5

10

15

20

aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr 245 250 255 260	1545
ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn 265 270 275	1593
aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala 280 285 290	1641
aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile 295 300 305	1689
ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys 310 315 320	1737
aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr 325 330 335 340	1785
gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val 345 350 355	1833
tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met 360 365 370	1881
tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp 375 380 385	1929
tct caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa Ser Gln Ala Ala Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys 390 395 400	1977
gcc gct gga gat gac agt gct gca gcg ctg gca gat gct cag aaa Ala Ala Gly Asp Asp Ser Ala Ala Ala Leu Ala Asp Ala Gln Lys 405 410 415 420	2025
gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gly Ile Leu 425 430 435	2073
aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val 440 445 450	2121

ctc ccg ctg cag caa gtt cta tgg atc cga gct cggt tac caa gct tac 2169
 Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg Tyr Gln Ala Tyr
 455 460 465

gta gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac 2217
 Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp
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cat cat cat cat cat cat tga 2238
 His His His His His His
 485 490

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 20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys
 35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala
 50 55 60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser
 65 70 75 80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr
 85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr
 100 105 110

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala
 115 120 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile
 130 135 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp
 145 150 155 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu
 165 170 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly
 180 185 190

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Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val
195 200 205

Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn
210 215 220

Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp
225 230 235 240

Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile
245 250 255

Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn
260 265 270

Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala
275 280 285

Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro
290 295 300

Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu
305 310 315 320

Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn
325 330 335

Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly
340 345 350

Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala
355 360 365

Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr
370 375 380

Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala
385 390 395 400

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Leu Ala
405 410 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln
420 425 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val
435 440 445

Ser Ala Gly Val Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg
450 455 460

Tyr Gln Ala Tyr Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
465 470 475 480

40014670-424401

21/22

Ser Ala Val Asp His His His His His His
485 490

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43

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35

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38

22/22

<210> 14
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<400> 14

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28

T-DNA T-22T-DNA T-DNA